

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: March 24, 2003, 15:46:23 ; Search time 13.9591 Seconds

(without alignments)
1225.145 Million cell updates/sec

Title: US-09-988-971-2_Copy_94_176

Perfect score: 446
Sequence: 1 WYEGLSREKAEILLPGN.....WLYSPRLTFFSLQALVDHY 83Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_Organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriophage:*
17: sp_archaeal:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	446	100.0	197	4 Q9H135	Q9H135 homo sapien
2	446	100.0	210	4 Q8WY18	Q8WY18 homo sapien
3	446	100.0	261	4 Q9H6Q3	Q9H6Q3 homo sapien
4	412	92.4	179	11 Q9D129	Q9D129 mus musculu
5	412	92.4	259	11 Q8V142	Q8V142 mus musculu
6	403	90.4	259	11 Q8R410	Q8R410 mus musculu
7	247	55.4	502	13 Q9DDK6	Q9DDK6 salmo salar
8	246	55.2	488	13 Q13064	Q13064 xenopus lae
9	243	54.5	151	4 Q9H8T7	Q9H8T7 homo sapien
10	243	54.5	276	4 Q13239	Q13239 homo sapien
11	240	53.8	280	11 Q8Q2X8	Q8Q2X8 mus musculu
12	240	53.8	281	11 Q8Q898	Q8Q898 mus musculu
13	232.5	52.1	505	4 Q961N1	Q961N1 homo sapien
14	228	51.1	509	6 Q95M32	Q95M32 hylobates s
15	227	50.9	509	11 Q91X65	Q91X65 mus musculu
16	220	49.3	509	6 Q95KR7	Q95KR7 salmistr sci

17	214	48.0	496	13 Q93411	Q93411 xenopus lae
18	211	47.3	502	13 Q8G5U9	Q8G5U9 tugu rubrip
19	211	47.3	541	11 Q99PW1	Q99PW1 ratius norv
20	207	46.4	812	15 Q85466	Q85466 y73 sarcoma
21	206	46.2	534	4 Q16248	Q16248 homo sapien
22	206	46.2	534	6 Q15M31	Q15M31 hylobates s
23	206	46.2	537	11 Q62844	Q62844 ratius norv
24	206	46.2	561	4 Q9UJ81	Q9UJ81 homo sapien
25	206	46.2	564	4 Q9UJ82	Q9UJ82 homo sapien
26	205	46.0	517	11 Q63206	Q63206 ratius norv
27	199	44.6	392	15 Q28414	Q28414 feline sarc
28	198.5	44.5	517	5 Q9V9J3	Q9V9J3 dirosophila
29	193.5	43.4	503	5 Q8WSU5	Q8WSU5 ephydactia f
30	186	41.7	523	15 Q85477	Q85477 rous sarcom
31	186	41.7	526	15 Q64994	Q64994 rous sarcom
32	186	41.7	526	15 Q93080	Q93080 rous sarcom
33	186	41.7	535	15 Q92857	Q92857 rous sarcom
34	183	41.0	587	15 Q64817	Q64817 avian sarco
35	181	40.6	526	15 Q64993	Q64993 rous sarcom
36	181	40.6	526	15 Q07461	Q07461 rous sarcom
37	179	40.1	545	15 Q86362	Q86362 rous sarcom
38	179	40.1	546	15 Q86363	Q86363 rous sarcom
39	177	39.7	110	15 Q9WK01	Q9WK01 rous sarcom
40	177	39.7	526	15 Q92806	Q92806 rous sarcom
41	177	39.7	542	11 Q93U10	Q93U10 ratius norv
42	176.5	39.6	496	11 Q923M5	Q923M5 mus musculu
43	176.5	39.6	527	5 Q9Y121	Q9Y121 ephydactia f
44	172	38.6	526	15 Q60567	Q60567 rous sarcom
45	168.5	37.8	488	4 Q9H3Y6	Q9H3Y6 homo sapien

ALIGNMENTS

RESULT 1	Q9H135	PRELIMINARY:	PRT:	197 AA.
ID	Q9H135			
AC	Q9H135			
DT	01-MAR-2001 (TREMBL)	16, Created		
DT	01-MAR-2001 (TREMBL)	16, Last sequence update		
DT	01-MAR-2002 (TREMBL)	20, Last annotation update		
DE	D9Y77B1.1 (Novel protein tyrosine kinase with Src homology domain 2 (SH2) domain) (Fragment).			
GN	D9Y77B1.1.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Theria; Primates; Carnivora; Hominoidea; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	LLOYD D.;			
RL	Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AL050318; CAB75365.1; -.			
DR	HSSP; P06239; ILK.			
DR	InterPro; IPR000980; SH2.			
DR	Pfam; PF00017; SH2.1.			
DR	PRINTS; PR00401; SH2DOMAIN.			
DR	ProDom; PD000093; SH2.1.			
DR	SMART; SM00252; SH2.1.			
DR	PROSITE; PS0001; SH2.1.			
FT	NON TER			
SQ	SEQUENCE 197 AA; 22124 MW; EF01FE7A85C5C1F1 CRC64;			
Query Match	100.0%;	Score 446;	DB 4;	Length 197;
Best Local Similarity	100.0%;	Pred. No. 2.5e-45;		
Matches	83;	Conservative	0;	Mismatches 0;
		Indels	0;	Gaps 0;
Qy	1 WYEGLSREKAEILLPGNPGAFILRESQTRSGYSLSVRLSPASWDRIRHYRINCL 60			
Db	30 WYEGLSREKAEILLPGNPGAFILRESQTRSGYSLSVRLSPASWDRIRHYRINCL 89			
Qy	61 DNGWLYSPRLTFFSLQALVDHY 83			

Db 90 DNGWLYISPRITFPSPQLVHDY 112

RESULT 2

ID 08WY18 PRELIMINARY; PRT; 210 AA.

DT 01-MAR-2002 (TREMBLrel. 20, Created)

DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)

DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)

DE Modulator of antigen receptor signaling, putative splice isoform

DE MARS-V.

OS Homo sapiens (Human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

OX NCBI_TaxID=9606;

RP SEQUENCE FROM N.A.

RC TISSUE=THYMUS;

RA Loreto M.P., McGlade C.J.;

RT "Modulator of Antigen Receptor Signaling (MARS) - putative splice

variant."

RT Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF290986; AAL38198.1; -.

DR InterPro; IPR000980; SH2.

DR InterPro; IPR001452; SH3.

DR Pfam; PF00017; SH2; 1.

DR Pfam; PF00018; SH3; 1.

DR PRINTS; PR00401; SH2DOMAIN.

DR PRINTS; PR00452; SH3DOMAIN.

DR PRODOM; PD000093; SH2; 1.

DR SMART; SM00252; SH2; 1.

DR SMART; SM00326; SH3; 1.

DR PROSITE; PSS0001; SH2; 1.

DR PROSITE; PSS0002; SH3; 1.

KW Receptor.

SO SEQUENCE 210 AA; 23103 MW; BED620853A472E CRC64;

Query Match 100.0%; Score 446; DB 4; Length 210;
Best Local Similarity 100.0%; Pred. No. 2, 7e-45;
Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WLYEGLSRKAEELLLPGNPGAFILRESOTRGSGYSVRLSRPASMDIRRHRIHCL 60

Db 94 WLYEGLSRKAEELLLPGNPGAFILRESOTRGSGYSVRLSRPASMDIRRHRIHCL 153

QY 61 DNGWLYISPRITFPSPQLVHDY 83

Db 154 DNGWLYISPRITFPSPQLVHDY 176

RESULT 3

ID 09H603 PRELIMINARY; PRT; 261 AA.

DT 01-MAR-2001 (TREMBLrel. 16, Created)

DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)

DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)

DE CDNA: FLJ21992.1, clone HEP06554 (Src-like adapter protein-2)

DE (Modulator of antigen receptor signaling MARS).

OS Homo sapiens (Human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

OX NCBI_TaxID=9606;

RP SEQUENCE FROM N.A.

RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,

RA Okitani R., Ota T., Suzuki Y., Okeyashi M., Nishi T., Shibahara T.,

RA Tanaka T., Nakamura Y., Isegaki T., Sugano S.,

RT "NEO human cDNA sequencing project."

RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=21553259; PubMed=11696592;

RA Holland S.J., Liao X.C., Mendenhall M.K., Zhou X., Pardo J., Chu P.,

RA Spencer C., Fu A.C., Sheng N., Yu P., Pali E., Nagin A., Shen M.,

RA Yu S., Chan E., Wu X., Li C., Moiseschlagner M., Aversa G.,

RA Kolbinger F., Bennett M.K., Moliniaux S., Luo Y., Payan D.G.,

RA Mancebo H.S.Y., Wu J.,

RT "Functional Cloning of Src-like Adapter Protein-2 (SLAP-2), a Novel

Inhibitor of Antigen Receptor Signaling."

RL J. Exp. Med. 194:1263-1276 (2001).

RN [3]

RP SEQUENCE FROM N.A.

RC TISSUE=THYMUS;

RA Loreto M.P., McGlade C.J.;

RT "Modulator of Antigen Receptor Signaling (MARS)";

RT Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.

CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.

DR EMBL; AK025645; BAB15201.1; -.

DR EMBL; AF290985; AAL38197.1; -.

DR HSP; P06239; ILK.

DR InterPro; IPR000980; SH2.

DR InterPro; IPR001452; SH3.

DR Pfam; PF00017; SH2; 1.

DR Pfam; PF00018; SH3; 1.

DR PRINTS; PR00401; SH2DOMAIN.

DR PRODOM; PD000093; SH2; 1.

DR SMART; SM00252; SH2; 1.

DR SMART; SM00326; SH3; 1.

DR PROSITE; PSS0001; SH2; 1.

DR PROSITE; PSS0002; SH3; 1.

KW SH3 domain; Receptor.

SO SEQUENCE 261 AA; 28585 MW; 858A034516723D CRC64;

Query Match 100.0%; Score 446; DB 4; Length 261;
Best Local Similarity 100.0%; Pred. No. 3, 4e-45;
Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WLYEGLSRKAEELLLPGNPGAFILRESOTRGSGYSVRLSRPASMDIRRHRIHCL 60

Db 94 WLYEGLSRKAEELLLPGNPGAFILRESOTRGSGYSVRLSRPASMDIRRHRIHCL 153

QY 61 DNGWLYISPRITFPSPQLVHDY 83

Db 154 DNGWLYISPRITFPSPQLVHDY 176

RESULT 4

ID 09D129 PRELIMINARY; PRT; 179 AA.

DT 01-JUN-2001 (TREMBLrel. 17, Created)

DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)

DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)

DE A930009E2IRIK protein.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=RETINA;

RA MEDLINE=21085660; PubMed=11217851;

RA Kawai U., Shinagawa A., Shidara K., Yoshino M., Itoh M., Ishii Y.,

RA Aikawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

RA Aikawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K.I.,

RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochwa H.,

RA Kuhl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Schirini L.M., Staudt F., Suzuki R., Tomita M., Wagner T., Washio T.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Baran G.,

RA Blake J., Boffelli D., Bojunga N., Caminci P., de Bona M.F.,
 RA Bromberg M.J., Bulc C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hoffman M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaez P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sabaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
 RA Hayashizaki Y.,
 RT "Functional annotation of a full-length mouse cDNA collection."
 RL Nucleic Acids Res. 30(2001).
 DR EMBL: AK020637, BA32223.1, -.
 DR HSSP: P06339, ILK.
 DR MGD: MG1:1925049, A93009E21R1K.
 DR InterPro: IPR000980, SH2.
 DR Pfam: PF00017, SH2.1.
 DR PRINTS: PR00401, SH2DOMAIN.
 DR Prodom: PD000093, SH2.1.
 DR SMART: SM00252, SH2.1.
 DR PROSITE: PS50001, SH2.1.
 SQ SEQUENCE 179 AA; 19926 MW; 60477A0CF4003FCD CRC64;

Query Match 92.4%; Score 412; DB 11; Length 179;
 Best Local Similarity 94.0%; Pred. No. 2, 6e-41;
 Matches 78; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 WYEGLSREKAEELLPPGCGAFILRESQTRGSGYSLVRLSPASWDRIRHYRIGL 60
 DB 13 WYEGLSREKAEELLPPGCGAFILRESQTRGSGYSLVRLSPASWDRIRHYRIGL 72
 DB 73 DNGWLYISPRITFSPSLALVDHY 83
 DB 73 DNGWLYISPRITFSPSLALVDHY 95

RESULT 5
 ID Q8V142 PRELIMINARY; PRT; 259 AA.

AC Q8V142;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Modulator of antigen receptor signaling MARS.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Loreto M.P., McGlade C.J.;
 RT "Modulator of Antigen Receptor Signaling (MARS)."
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF287467, ALJ8196.1, -.
 DR InterPro: IPR000980, SH2.
 DR InterPro: IPR001452, SH3.
 DR Pfam: PF00017, SH2.1.
 DR Pfam: PF00018, SH3.1.
 DR PRINTS: PR00401, SH2DOMAIN.
 DR Prodom: PD000093, SH2.1.
 DR SMART: SM00252, SH2.1.
 DR SMART: SM00326, SH3.1.
 DR PROSITE: PS50001, SH2.1.
 DR PROSITE: PS50002, SH3.1.
 KW Receptor.
 SQ SEQUENCE 259 AA; 28476 MW; 8270F17CD3FC50A3 CRC64;

Query Match 92.4%; Score 412; DB 11; Length 259;
 Best Local Similarity 94.0%; Pred. No. 3, 9e-41;
 Matches 78; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 WYEGLSREKAEELLPPGCGAFILRESQTRGSGYSLVRLSPASWDRIRHYRIGL 60
 DB 13 WYEGLSREKAEELLPPGCGAFILRESQTRGSGYSLVRLSPASWDRIRHYRIGL 72
 DB 73 DNGWLYISPRITFSPSLALVDHY 83
 DB 73 DNGWLYISPRITFSPSLALVDHY 95

DB 93 WYEGLSREKAEELLPPGCGAFILRESQTRGSGYSLVRLSPASWDRIRHYRIGL 152
 QY 61 DNGWLYISPRITFSPSLALVDHY 83
 DB 153 DNGWLYISPRITFSPSLALVDHY 175

RESULT 6

ID Q8R4L0 PRELIMINARY; PRT; 259 AA.
 AC Q8R4L0;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Src-like adapter protein-2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Pandey A., Ibarrol N., Kratchmarova I., Fernandez M.,
 RA Constantinescu S., Ohara O., Sawasdi Kosol S., Lodish H.F., Mann M.;
 RT "A novel Src homology 2 domain-containing molecule, Src-Like Adapter
 Protein-2 (SLAP-2), which negatively regulates T cell receptor
 signaling."
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Ibarrol N., Mann M., Pandey A.;
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF434990, ALB6403.1, -.
 SQ SEQUENCE 259 AA; 28516 MW; 1388E68244152E34 CRC64;

Query Match 90.4%; Score 403; DB 11; Length 259;
 Best Local Similarity 92.8%; Pred. No. 4, 7e-40;
 Matches 77; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 WYEGLSREKAEELLPPGCGAFILRESQTRGSGYSLVRLSPASWDRIRHYRIGL 60
 DB 93 WYEGLSREKAEELLPPGCGAFILRESQTRGSGYSLVRLSPASWDRIRHYRIGL 152
 QY 61 DNGWLYISPRITFSPSLALVDHY 83
 DB 153 DNGWLYISPRITFSPSLALVDHY 175

RESULT 7

ID Q9DDK6 PRELIMINARY; PRT; 502 AA.
 AC Q9DDK6;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Src-family tyrosine kinase SKC.
 OS Salmo salar (Atlantic salmon).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei.
 OC Proacanthopterygii; Salmoniformes; Salmonidae; Salmo.
 OX NCBI_TaxId=8030;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Hordvik I., Male R.;
 RT "A leukocyte cDNA of Atlantic salmon encoding a Src-family tyrosine
 kinase."
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 CC -1 SIMILARITY: CONTRAST 1 SH3 DOMAIN.
 DR EMBL: AF221110, AAG38611.1, -.
 DR HSSP: P08631, IAD5.
 DR InterPro: IPR000719, Euk_pkinase.
 DR InterPro: IPR002290, Ser_thr_pkinase.
 DR InterPro: IPR000980, SH2.
 DR InterPro: IPR001452, SH3.

RESULT 6		
OI3064	PRELIMINARY;	PRT; 488 AA.
ID OI3064		
AC OI3064;		
DT 01-JUL-1997 (TRENDELrel, 04, Created)		
DT 01-JUL-1997 (TRENDELrel, 04, last sequence update)		
DT 01-MAR-2002 (TRENDELrel, 20, last annotation update)		
DE lyn protein tyrosine kinase.		
GN lyn.		
OS Xenopus laevis (African clawed frog).		
OC Eumetazoa; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;		
OC Xenopodinae; Xenopus.		
OX NCBI_TaxId=8355;		
RN [1]		
RP SEQUENCE FROM N.A.		
RA Fukami Y., Funabiki K., Sato K.;		
RT "Nucleotide sequence of Xenopus lyn protein tyrosine kinase.";		
RL Submitted (APR-1997) to the EMBL/GenBank/DDAI databases.		
CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.		
DR EMBL: AB003358; BAA20078.1; "-."		
DR HSSP: P08631; IAD5.		
DR InterPro: IPRO00719; Euk_Dkinase.		
DR InterPro: IPRO00980; SH2.		
DR InterPro: IPRO01452; SH3.		
DR InterPro: IPRO01245; Tyr_kinase.		
DR Pfam: PF00069; kinase.1.		
DR Pfam: PF00017; SH2.1.		
DR Pfam: PF00018; SH3.1.		
DR PRINTS: PR00401; SH3DOMAIN.		
DR PRINTS: PR00452; SH3DOMAIN.		
DR PRINTS: PRO0109; TYRKINASE.		
DR ProDom: PD000001; Euk_dkinase.1.		
DR ProDom: PD000066; SH3.1.		
DR ProDom: PD000093; SH2.1.		
DR SMART: SM00252; SH2.1.		
DR SMART: SM00326; SH3.1.		
DR SMART: SM00219; TyrcK.1.		

RESULT 9		
09HB17	ID	09HB17
	PRELIMINARY;	PRT; 161 AA.
AC	09HB17;	
DT	01-MAR-2001 (TREMBlrel. 16, Created)	
DT	01-MAR-2001 (TREMBlrel. 16, Last sequence update)	
DT	01-JUN-2002 (TREMBlrel. 21, Last annotation update)	
DE	Src-like adapter protein (Fragment).	
OS	Homo sapiens (Human).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.	
OX	NCBI_taxid=9606;	

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RA Blöschsmidt K., Kalaydjieva L., Goodman R., Griesan U., Haas F.,
RA Jorges, Rd, Schilhabel M.B., Menzel U., Dette M.D., Baumgart C.,
RA Jahn N., Rosenthal A.;
RL "Chromosome 8 genomic sequence.";
RT Submitted (Apr-2000) to the EMBL/GenBank/DBJ databases.
RN (2)
RP SEQUENCE FROM N.A.
RA Genome Sequencing Center Jena;
RI Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
CC -1 SIMILARITY: CONTAINS 1 SH3 DOMAIN.
DR EMBL: AF235100; AAC29878.1; -.
DR HSSP: P08631; 3HCK
DR InterPro: IPR000980; SH2.
DR InterPro: IPR001432; SH3.
DR Pfam: PF00017; SH2; 1.
DR Pfam: PF00018; SH3; 1.
DR PRINTS: PR00401; SH2DOMAIN.
DR ProDom: PD000093; SH2; 1.
DR SMART: SM00252; SH2.1.
DR SMART: SM00325; SH3.1.
DR PROSITE: PS50001; SH2; 1.
DR PROSITE: PS50002; SH3; 1.
DR SH3 domain.
KW FT NON TER. 161
SQ SEQUENCE 161 AA; 18493 MW; FC28546680AEB20 CRC64;

Query_March 54.5%; Score 243; DB 4; Length 161;
Best local Similarity 57.8%; Pred. No. 3, 6e-21;
Matches 46; Conservative 12; Mismatches 17; Indels 6; Gaps

Qy 1 WLVEGLSRKEAEELLPLGNPGAGFLIFESQTRRGYSISLVLSRPMASDRIRHYINCL 60
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 84 WLFEGLRDPAEELLOTJEDTKVSFWIRESEETKGFYSIVR-----HROGVHYRIFRL 137
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Qy 61 DNGGLYISPLTFPSLAQVDHY 83
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 138 ENMYIYISPLTFQCLELVNHY 160
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

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RESULT 10
ID 013239 PRELIMINARY; PRT; 276 AA.

AC 013239
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Putative SRC-like adapter protein (SLAP) (SRC-like-adapter).
GN SLAP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96423054; PubMed=8825655;
RA Angrist M., Wells D.E., Chakravarti A., Pandey A.;
RT "Chromosomal localization of the mouse Src-like adapter protein (Slap)
RT gene and its putative human homolog SLA.",
RL Genomics 30:623-625(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RA Weijerink P.H.S., Zorn G., Bikker H., Bolhuis P.A., Baas F.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Ohtsuki T., Hatake K., Ikeda M., Tomizuka H., Terui Y., Uwat M.,
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Blechschmidt K., Kalaydjieva L., Goodman R., Gresham D., Baas F.,
RA Jonge, Rd., Schilhabel M., Wen G., Menzel U., Dettle M., Baumgart C.,
RA Rosenthal A.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RC TISSUE=BONE MARROW;
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
DR EMBL; U30473; AAC50357.1; -;
DR EMBL; U44403; AAC27662.1; -;
DR EMBL; D89077; BA13758.1; -;
DR EMBL; AF305872; AAC17933.1; -;
DR EMBL; BC007042; AAH07042.1; -;
DR HSSP; P08631; JHCK.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR001452; SH3.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF00018; SH3; 1.
DR PRINTS; PR00401; SH2DOMAIN.
DR PRODOM; PD000093; SH2; 1.
DR SMART; SM00252; SH2; 1.
DR SMART; SM00326; SH3; 1.
DR PROSITE; PS50001; SH2; 1.
DR PROSITE; PS50002; SH3; 1.
KW SH3 domain.
SQ SEQUENCE 276 AA; 31156 MW; B0FC07D7B2ECA378 CRC64;

Query Match 54.8%; Score 243; DB 4; Length 276;
Best Local Similarity 57.8%; Pred. No. 6, 7e-21;
Matches 48; Conservative 12; Mismatches 17; Indels 6; Gaps 1;

QY 1 WLVEGLSREKAEELLPLPGNGAFILRESQTRGSGSLVRLSPRSMRIRRHRIHCL 60
DB 84 WLFEGLGRDAEELQLPDTKXGFMIRESETKKGYSLSR-----HGVKRIIRRL 137
QY 61 DNGMLYISPLRTPPSIQALVDHY 83
DB 138 PNMWYISPLRTPFOCLEDLVNHV 160

RESULT 11

ID 080ZX8 PRELIMINARY; PRT; 280 AA.

AC 080ZX8
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Src-like adapter protein SLAP (Fragment).
GN Mus musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ILS, AND ISS;
RX MEDLINE=21363810; PubMed=11471062;
RA Ehringer M.A., Thompson J., Conroy O., Xu Y., Yang F., Canniffe J.,
RA Beeson M., Gordon L., Bennett B., Johnson T.E., Sikela J.M.;
RT "High-throughput sequence identification of gene coding variants
RT within alcohol-related QTLs.",
RL Mamm. Genome 12:657-663(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=ILS, AND ISS;
RA Ehringer M.A., Thompson J., Conroy O., Xu Y., Yang F., Canniffe J.,
RA Beeson M., Gordon L., Bennett B., Johnson T.E., Sikela J.M.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY079449; AAL87537.1; -;
DR EMBL; AY079450; AAL87538.1; -;
FT NON TER 1
FT NON TER 1
FT NON TER 1
SQ SEQUENCE 280 AA; 31549 MW; A05C3BF7FEAD951 CRC64;

Query Match 53.8%; Score 240; DB 11; Length 280;
Best Local Similarity 57.8%; Pred. No. 1, 6e-20;
Matches 48; Conservative 11; Mismatches 18; Indels 6; Gaps 1;

QY 1 WLVEGLSREKAEELLPLPGNGAFILRESQTRGSGSLVRLSPRSMRIRRHRIHCL 60
DB 83 WLFEGLGRDAEELQLPDTKXGFMIRESETKKGYSLSR-----HGVKRIIRRL 136
QY 61 DNGMLYISPLRTPPSIQALVDHY 83
DB 137 PNMWYISPLRTPFOCLEDLVNHV 159

RESULT 12

ID 060898 PRELIMINARY; PRT; 281 AA.

AC 060898
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE SRC-like adapter protein.
GN SLA OR SLAP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95370243; PubMed=7543898;
RA Pandey A., Duan H., Dixit V.M.;
RT "Characterization of a novel Src-like adapter protein that associates
RT with the Eck receptor tyrosine kinase.",
RL J Biol. Chem. 270:19201-19204(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20033985; PubMed=10630289;
RA Carrier A., Nguyen C., Victorero G., Granjeaud S., Rocha D.,
RA Bernard K., Miazek A., Ferrier P., Wallsten M., Naquet P.,

RA Malissen B., Jordan B.;
 RT "differential gene expression in CD3e- and RAG1-deficient thymuses:
 RT definition of a set of genes potentially involved in thymocyte
 RT maturation.";
 RL Immunogenetics 50:255-270(1999).
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
 DR EMBL: U29056; AAA82756.1; -.
 DR EMBL: AJ131777; CAB6139.1; -.
 DR HSSP: p16277; 1BLK.
 DR MED: MG1:104295; Sla.
 DR InterPro: IPR000980; SH2.
 DR InterPro: IPR001452; SH3.
 DR Pfam: PF00017; SH2; 1.
 DR Pfam: PF00018; SH3; 1.
 DR PRINTS: PR00401; SH2DOMAIN.
 DR ProDom: PD000093; SH2; 1.
 DR SMART: SM00252; SH2; 1.
 DR SMART: SM00326; SH3; 1.
 DR PROSITE: PS50001; SH2; 1.
 DR PROSITE: PS50002; SH3; 1.
 DR SH3 domain.
 SQ SEQUENCE 281 AA; 31680 MW; B347921656A74D1 CRC64;

Query Match 53.8%; Score 240; DB 11; Length 281;
 Best Local Similarity 57.8%; Pred. No. 1.6e-20;
 Matches 48; Conservative 11; Mismatches 18; Indels 6; Gaps 1;

QY 1 WLYEGLSRKAEELLPLPGNGAFILRESQRRGSYSLSVRLSPASWDRIHRYRHCL 60
 DB 84 WLYEGLSRKAEELLPLPGNGAFILRESQRRGSYSLSVRLSPASWDRIHRYRHCL 60
 QY 61 DNGWLYSPRLTFPSLQALVDHY 83
 DB 138 PNMWYISPRITFPGHELVYHY 160

RESULT 13

ID Q96IN1 PRELIMINARY; PRT; 505 AA.
 AC Q96IN1;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Unknown (protein for MG:16168).
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-LYMPH.
 RA Struhsberg R.;
 RL Submitted (Mar-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC007371; AA07371.1; -.
 DR InterPro: IPR000719; Euk_Pkinase.
 DR InterPro: IPR000980; SH2.
 DR InterPro: IPR001452; SH3.
 DR Pfam: PF00069; Pkinase; 1.
 DR Pfam: PF00017; SH2; 1.
 DR Pfam: PF00018; SH3; 1.
 DR ProDom: PD000001; Euk_Pkinase; 1.
 DR ProDom: PD000066; SH2; 1.
 DR ProDom: PD000093; SH3; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1;
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS50001; SH2; 1.
 DR PROSITE: PS50002; SH3; 1.
 DR ATP-binding; Transferase.
 KM SEQUENCE 505 AA; 57706 MW; B5F739BEF8389176 CRC64;
 SQ

Query Match 52.1%; Score 232.5; DB 4; Length 505;
 Best Local Similarity 54.2%; Pred. No. 2.5e-19;
 Matches 45; Conservative 13; Mismatches 24; Indels 1; Gaps 1;

QY 1 WLYEGLSRKAEELLPLPGNGAFILRESQRRGSYSLSVRLSPASWDRIHRYRHCL 60
 DB 124 WLYEGLSRKAEELLPLPGNGAFILRESQRRGSYSLSVRLSPASWDRIHRYRHCL 182
 QY 61 DNGWLYSPRLTFPSLQALVDHY 83
 DB 183 DNGWLYSPRLTFPSLQALVDHY 205

RESULT 14

ID Q95M32 PRELIMINARY; PRT; 509 AA.
 AC Q95M32;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Lck protein.
 GN LCK.
 OS Hylobates sp. (gibbon).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
 NCBI_TaxID=9581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Picard C.;
 RL Thesis (2001), Department of Experimental Oncology Laboratory, U.
 DR EMBL: AJ320182; CAC44027.1; -.
 DR InterPro: IPR000719; Euk_Pkinase.
 DR InterPro: IPR000980; SH2.
 DR InterPro: IPR001452; SH3.
 DR InterPro: IPR001245; Tyr_Pkinase.
 DR Pfam: PF00069; Pkinase; 1.
 DR Pfam: PF00017; SH2; 1.
 DR Pfam: PF00018; SH3; 1.
 DR ProDom: PD000001; Euk_Pkinase; 1.
 DR ProDom: PD000066; SH2; 1.
 DR ProDom: PD000093; SH3; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS50001; SH2; 1.
 DR PROSITE: PS50002; SH3; 1.
 DR ATP-binding; Transferase.
 KM SEQUENCE 509 AA; 57946 MW; F1BF5C237C8D87E CRC64;
 SQ

Query Match 51.1%; Score 228; DB 6; Length 509;
 Best Local Similarity 54.2%; Pred. No. 8.6e-19;
 Matches 45; Conservative 12; Mismatches 26; Indels 0; Gaps 0;

QY 1 WLYEGLSRKAEELLPLPGNGAFILRESQRRGSYSLSVRLSPASWDRIHRYRHCL 60
 DB 127 WLYEGLSRKAEELLPLPGNGAFILRESQRRGSYSLSVRLSPASWDRIHRYRHCL 186
 QY 61 DNGWLYSPRLTFPSLQALVDHY 83
 DB 187 DNGWLYSPRLTFPSLQALVDHY 209

RESULT 15

ID Q91X65 PRELIMINARY; PRT; 509 AA.
 AC Q91X65;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Similar to lymphocyte-specific protein tyrosine kinase.
 GN LCK.
 OS Mus musculus (mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]

RP SEQUENCE FROM N. A.
 RC TISSUE-SALIVARY GLAND;
 RA Strausberg R.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC011474; AAH11474.1; -
 DR MGI; MGI:96756; Lck.
 DR InterPro; IPR000719; Euk_pkinase.
 DR InterPro; IPR000980; SH2.
 DR InterPro; IPR001452; SH3.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR Pfam; PF00069; pkinase; 1.
 DR Pfam; PF00017; SH2; 1.
 DR Pfam; PF00018; SH3; 1.
 DR ProDom; PD000001; Euk_pkinase; 1.
 DR ProDom; PD000066; SH3; 1.
 DR ProDom; PD000093; SH2; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
 DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; UNKNOWN_1.
 DR PROSITE; PS00021; SH2; 1.
 DR PROSITE; PS00022; SH3; 1.
 KW ATP-binding; Kinase; Transferase.
 SQ SEQUENCE 509 AA; 57942 MW; 3513102F49A7FD08 CRC64;

Query Match 50.9%; Score 227; DB 11; Length 509;
 Best Local Similarity 54.2%; Pred. No. 1,1e-18;
 Matches 45; Conservative 12; Mismatches 26; Indels 0; Gaps 0;
 QY 1 WYEGISREKAEELLIPGPGAPLIREQTRRGYSLSVRLSRPASMDRIRHYRIHCL 60
 Db 127 WFKNLISRKDAERQLAPGNTGSGFLIRESESTAGSFLSVRDPDQNGEVVKKYKIRNL 186
 QY 61 DNGWLYISPRLTFFPSIQALVDHY 83
 Db 187 DNGGFYISPRITFFGRLHDLVRYH 209

Search completed: March 24, 2003, 15:50:36
 Job time: 14.9591 secs

